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OIPE

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 3 <110> APPLICANT: Vernet, Cornie AM
 4         Fernandes, Elma
 5         Shimkets, Richard A
 6         Herrmann, John L
 7         Majumder, Kumud
 8         Mishra, Vishna
 9         Mezes, Peter S
10         Rastelli, Luca
12 <120> TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
14 <130> FILE REFERENCE: 15966-697
16 <140> CURRENT APPLICATION NUMBER: 09/800198
17 <141> CURRENT FILING DATE: 2001-03-05
19 <150> PRIOR APPLICATION NUMBER: 60/186,596 ,
20 <151> PRIOR FILING DATE: 2000-03-03
22 <160> NUMBER OF SEQ ID NOS: 98
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 771
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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33 <222> LOCATION: (438)..(752)
35 <400> SEQUENCE: 1
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40 attggcagcc ttagaactag tgggaaggcg ggtgcgcgaa gtcgaggggc ggagagaggg 180
42 ggccggagga gctgctttct gaatccaagt tcgtgggctc tctcagaagt cctcaggacg 240
44 gagcagaggt ggccggcggg cccggctgac tgcgcctctg ctttctttcc ataacctttt 300
46 ctttcggact cgaatcacgg ctgctgcgaa gggtctagtt ccggacacta gggccccaga 360
48 tcgtgtcaca tccatatgac acttggaatg tgacagggca ggatgtgatc tttggctgtg 420
50 aagtgtttgc ctacccc atg gcc tcc atc gag tgg agg aag gat ggc ttg     470
51                    Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu
52                     1               5                  10
54 gac atc cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg     518
55 Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg
56           15              20                  25
58 ggt gga ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct     566
59 Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala
60           30              35                  40
62 gtg cgt ccc agt gat gag ggc act tac cgc tgc ctt gcc cgc aat gcc     614
63 Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Ala Arg Asn Ala
64       45              50                  55
66 ctg ggt caa gtg gag gcc cct gct agc ttg aca gtg ctc aca cct gac     662
67 Leu Gly Gln Val Glu Ala Pro Ala Ser Leu Thr Val Leu Thr Pro Asp
68 60                65                  70                  75
70 cag ctg aac tct aca ggc atc ccc cag ctg cga tca cta aac ctg gtt     710
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                RAW SEQUENCE LISTING                    DATE: 10/29/2001
                PATENT APPLICATION:  US/09/800,198      TIME: 15:42:22

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                Output Set: N:\CRF3\10292001\I800198.raw
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71 Gln Leu Asn Ser Thr Gly Ile Pro Gln Leu Arg Ser Leu Asn Leu Val
72                   80                  85                  90
74 cct gag gag gag gct gag agt gaa gag aat gac gat tac tac          752
75 Pro Glu Glu Glu Ala Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
76                   95                  100                 105
78 taggtccaga gctctggcc                                             771
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 105
83 <212> TYPE: PRT
84 <213> ORGANISM: Homo sapiens
86 <400> SEQUENCE: 2
87 Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu Asp Ile Gln Leu Pro
88   1               5                  10                  15
90 Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly Pro Gln Arg
91                   20                  25                  30
93 Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg Pro Ser Asp
94                   35                  40                  45
96 Glu Gly Thr Tyr Arg Cys Leu Ala Arg Asn Ala Leu Gly Gln Val Glu
97        50                  55                  60
99 Ala Pro Ala Ser Leu Thr Val Leu Thr Pro Asp Gln Leu Asn Ser Thr
100  65                  70                  75                  80
102 Gly Ile Pro Gln Leu Arg Ser Leu Asn Leu Val Pro Glu Glu Glu Ala
103                  85                  90                  95
105 Glu Ser Glu Glu Asn Asp Asp Tyr Tyr
106                  100                 105
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111 <211> LENGTH: 5502
112 <212> TYPE: DNA
113 <213> ORGANISM: Homo sapiens
115 <220> FEATURE:
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122 actagtaacg gccgccagtg tgctggaatt cggcttactc actatagggc tcgagcggct 120
124 gcccgggcag gtcattaatt ccatttcttt ttagagtatc acagctttct ccttcactga 180
126 ccacccttg cttcctgtca gaaagccctg gacagaactc tctgtgggat tctgcccatg 240
128 tttctgagat atcgcctcaa ttgtcctggc tgggctgtcg ggtctgcccg ttttacagat 300
130 gggcaaactg gagtgggaag tatccgggtg gcttcctcag gcctgcagct ggtggagcag 360
132 ctactgaaac aatcaggagc ccagaagctt tgaagtcaca agaagagaag actcccaga 419
134 atg cag tgt gat gtt ggt gat gga cgc ctg ttt cgc ctt tca ctt aaa 467
135 Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys
136   1               5                  10                  15
138 cgt gcc ctt tcc agc tgc cct gac ctc ttt ggg ctt tcc agc cgc aac 515
139 Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn
140                  20                  25                  30
142 gag ctg ctg gcc tcc tgc ggg aag aag ttc tgc agc cga ggg agc cgg 563
143 Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg
144                  35                  40                  45
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RAW SEQUENCE LISTING   DATE: 10/29/2001
PATENT APPLICATION: US/09/800,198   TIME: 15:42:22

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Output Set: N:\CRF3\10292001\I800198.raw

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146 tgc gtg ctc agc agg aag aca ggg gag ccc gaa tgc cag tgc ctg gag    611
147 Cys Val Leu Ser Arg Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu
148     50                  55                  60
150 gca tgc agg ccc agc tac gtg cct gtg tgc ggc tct gat ggg agg ttt    659
151 Ala Cys Arg Pro Ser Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe
152  65                  70                  75                  80
154 tat gaa aac cac tgt aag ctc cac cgt gct gct tgc ctc ctg gga aag    707
155 Tyr Glu Asn His Cys Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys
156                     85                  90                  95
158 agg atc acc gtc atc cac agc aag gac tgt ttc ctc aaa ggt gac acg    755
159 Arg Ile Thr Val Ile His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr
160                     100                 105                 110
162 tgc acc atg gcc ggc tac gcc cgc ttg aag aat gtc ctt ctg gca ctc    803
163 Cys Thr Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu
164         115                 120                 125
166 cag acc cgt ctg cag cca ctc caa gaa gga gac agc aga caa gac cct    851
167 Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro
168         130                 135                 140
170 gcc tcc cag aag cgc ctc ctg gtg gaa tct ctg ttc agg gac tta gat    899
171 Ala Ser Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp
172 145                 150                 155                 160
174 gca gat ggc aat ggc cac ctc agc agc tcc gaa ctg gct cag cat gtg    947
175 Ala Asp Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val
176                     165                 170                 175
178 ctg aag aag cag gac ctg gat gaa gac tta ctt ggt tgc tca cca ggt    995
179 Leu Lys Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly
180                     180                 185                 190
182 gac ctc ctc cga ttt gac gat tac aac agt gac agc tcc ctg acc ctc    1043
183 Asp Leu Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu
184         195                 200                 205
186 cgc gag ttc tac atg gcc ttc caa gtg gtt cag ctc agc ctc gcc ccc    1091
187 Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro
188     210                 215                 220
190 gag gac agg gtc agt gtg acc aca gtg acc gtg ggg ctg agc aca gtg    1139
191 Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val
192 225                 230                 235                 240
194 ctg acc tgc gcc gtc cat gga gac ctg agg cca cca atc atc tgg aag    1187
195 Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys
196                     245                 250                 255
198 cgc aac ggg ctc acc ctg aac ttc ctg gac ttg gaa gac atc aat gac    1235
199 Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp
200                     260                 265                 270
202 ttt gga gag gat gat tcc ctg tac atc acc aag gtg acc acc atc cac    1283
203 Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His
204         275                 280                 285
206 atg ggc aat tac acc tgc cat gct tcc ggc cac gag cag ctg ttc cag    1331
207 Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln
208         290                 295                 300
210 acc cac gtc ctg cag gtg aat gtg ccg cca gtc atc cgt gtc tat cca    1379
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RAW SEQUENCE LISTING
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212 305                 310                 315                 320
214 gag agc cag gca cag gag cct gga gtg gca gcc agc cta aga tgc cat   1427
215 Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His
216             325                 330                 335
218 gct gag ggc att ccc atg ccc aga atc act tgg ctg aaa aac ggc gtg   1475
219 Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val
220             340                 345                 350
222 gat gtc tca act cag atg tcc aaa cag ctc tcc ctt tta gcc aat ggg   1523
223 Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly
224             355                 360                 365
226 agc gaa ctc cac atc agc agt gtt cgg tat gaa gac aca ggg gca tac   1571
227 Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr
228     370                 375                 380
230 acc tgc att gcc aaa aat gaa gtg ggt gtg gat gaa gat atc tcc tcg   1619
231 Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser
232 385                 390                 395                 400
234 ctc ttc att gaa gac tca gct aga aag acc ctt gca aac atc ctg tgg   1667
235 Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp
236             405                 410                 415
238 cga gag gaa ggc ctc agc gtg gga aac atg ttc tat gtc ttc tcc gac   1715
239 Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp
240             420                 425                 430
242 gac ggt atc atc gtc atc cat cct gtg gac tgt gag atc cag agg cac   1763
243 Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His
244             435                 440                 445
246 ctc aaa ccc acg gaa aag att ttc atg agc tat gaa gaa atc tgt cct   1811
247 Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro
248     450                 455                 460
250 caa aga gaa aaa aat gca acc cag ccc tgc cag tgg gta tct gca gtc   1859
251 Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val
252 465                 470                 475                 480
254 aat gtc cgg aac cgg tac atc tat gtg gcc cag cca gca ctg agc aga   1907
255 Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg
256             485                 490                 495
258 gtc ctt gtg gtc gac atc caa gcc cag aaa gtc cta cag tcc ata ggt   1955
259 Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly
260             500                 505                 510
262 gtg gac cct ctg ccg gct aag ctg tcc tat gac aag tca cat gac caa   2003
263 Val Asp Pro Leu Pro Ala Lys Leu Ser Tyr Asp Lys Ser His Asp Gln
264     515                 520                 525
266 gtg tgg gtc ctg agc tgg ggg gac gtg cac aag tcc cga cca agt ctc   2051
267 Val Trp Val Leu Ser Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu
268     530                 535                 540
270 cag gtg atc aca gaa gcc agc acc ggc cag agc cag cac ctc atc cgc   2099
271 Gln Val Ile Thr Glu Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg
272 545                 550                 555                 560
274 aca ccc ttt gca gga gtg gat gat ttc ttc att ccc cca aca aac ctc   2147
275 Thr Pro Phe Ala Gly Val Asp Asp Phe Phe Ile Pro Pro Thr Asn Leu
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 276                565               570               575
 278 atc atc aac cac atc agg ttt ggc ttc atc ttc aac aag tct gat cct 2195
 279 Ile Ile Asn His Ile Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro
 280                580               585               590
 282 gca gtc cac aag gtg gac ctg gaa aca atg atg ccc ctc aag acc atc 2243
 283 Ala Val His Lys Val Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile
 284                595               600               605
 286 ggc ctg cac cac cat ggc tgc gtg ccc cag gcc atg gca cac acc cac 2291
 287 Gly Leu His His His Gly Cys Val Pro Gln Ala Met Ala His Thr His
 288                610               615               620
 290 ctg ggc ggc tac ttc ttc atc cag tgc cga cag gac agc ccc gcc tct 2339
 291 Leu Gly Gly Tyr Phe Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser
 292 625                630               635               640
 294 gct gcc cga cag ctg ctc gtt gac agt gtc aca gac tct gtg ctt ggc 2387
 295 Ala Ala Arg Gln Leu Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly
 296                645               650               655
 298 ccc aat ggt gat gta aca ggc acc cca cac aca tcc ccc gac ggg cgc 2435
 299 Pro Asn Gly Asp Val Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg
 300                660               665               670
 302 ttc ata gtc agt gct gca gct gac agc ccc tgg ctg cac gtg cag gag 2483
 303 Phe Ile Val Ser Ala Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu
 304                675               680               685
 306 atc aca gtg cgg ggc gag atc cag acc ctg tat gac ctg caa ata aac 2531
 307 Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn
 308                690               695               700
 310 tcg ggc atc tca gac ttg gcc ttc cag cgc tcc ttc act gaa agc aat 2579
 311 Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn
 312 705                710               715               720
 314 caa tac aac atc tac gcg gct ctg cac acg gag ccg gac ctg ctg ttc 2627
 315 Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe
 316                725               730               735
 318 ctg gag ctg tcc acg ggg aag gtg ggc atg ctg aag aac tta aag gag 2675
 319 Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu
 320                740               745               750
 322 cca ccc gca ggg cca gct cag ccc tgg ggg ggt acc cac aga atc atg 2723
 323 Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met
 324                755               760               765
 326 agg gac agt ggg ctg ttt gga cag tac ctc ctc aca cca gcc cga gag 2771
 327 Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu
 328 770                775               780
 330 tca ctg ttc ctc atc aat ggg aga caa aac acg ctg cgg tgt gag gtg 2819
 331 Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val
 332 785                790               795               800
 334 tca ggt ata aag ggg ggg acc aca gtg gtg tgg gtg ggt gag gta     2864
 335 Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val
 336                805               810               815
 338 tgaagggccc agagcagagc cctgggccaa ggaacacccc ctagtcctga cactgcagcc 2924
 340 tcaagcaggt acgctgtaca tttttacaga caaaagcaaa aacctgtact cgctttgtgg 2984
 342 ttcaacactg gtctccttgc aagtttccta gtataaggta tgcgctgcta ccaagattgg 3044
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VERIFICATION SUMMARY   DATE: 10/29/2001
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